

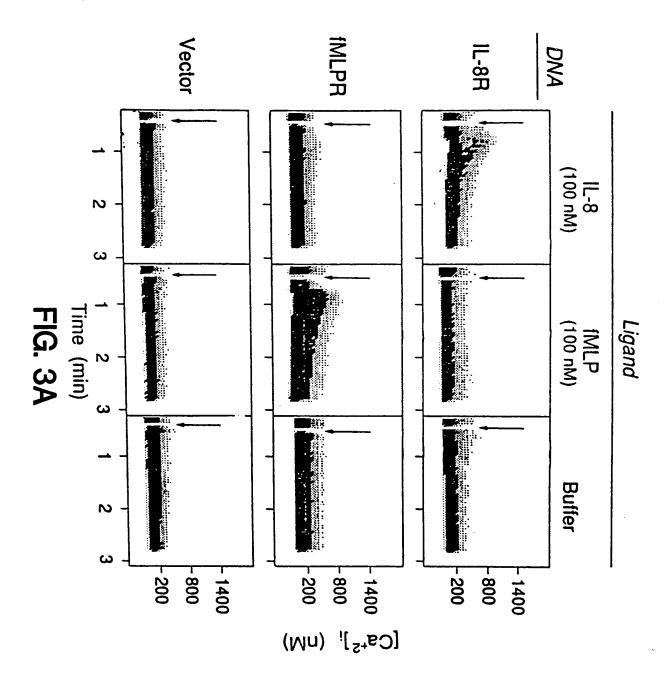
	ATG M t 1	TCA Ser	AAT Asn	ATT Ile	ACA Thr 5	GAT Asp	CCA Pro	CAG Gln	ATG Met	TGG Trp 10	GAT Asp	TTT Phe	86
GAT Asp	GAT Asp	CTA Leu 15	AAT Asn	TTC Phe	ACT Thr	GGC Gly	ATG Met 20	CCA Pro	CCT Pro	GCA Ala	GAT Asp	GAA Glu 25	125
GAT Asp	TAC Tyr	AGC Ser	CCC	TGT Cys 30	ATG Met	CTA Leu	GAA Glu	ACT Thr	GAG Glu 35	ACA Thr	CTC Leu	AAC Asn	164
AAG Lys	TAT Tyr 40	GTT Val	GTG Val	ATC Ile	ATC Ile	GCC Ala 45	TAT Tyr	GCC Ala	CTA Leu	GTG Val	TTC Phe 50	CTG Leu	203
CTG Leu	AGC Ser	CTG Leu	CTG Leu 55	GGA Gly	AAC Asn	TCC Ser	CTG Leu	GTG Val 60	ATG Met	CTG Leu	GTC Val	ATC Ile	242
TTA Leu 65	TAC Tyr	AGC Ser	AGG Arg	GTC Val	GGC Gly 70	CGC Arg	TCC Ser	GTC Val	ACT Thr	GAT Asp 75	GTC Val	TAC Tyr	281
CTG Leu	CTG Leu	AAC Asn 80	CTG Leu	GCC Ala	TTG Leu	GCC Ala	GAC Asp 85	CTA Leu	CTC Leu	TTT Phe	GCC Ala	CTG Leu 90	320
ACC Thr	TTG Leu	CCC Pro	ATC Ile	TGG Trp 95	GCC Ala	GCC Ala	TCC Ser	AAG Lys	GTG Val 100	AAT Asn	GGC Gly	TGG Trp	359
ATT Ile	TTT Phe 105	GGC Gly	ACA Thr	TTC Phe	CTG Leu	TGC Cys 110	AAG Lys	GTG Val	GTC Val	TCA Ser	CTC Leu 115	CTG Leu	398
AAG Lys	GAA Glu	GTC Val	AAC Asn 120	TTC Phe	TAC Tyr	AGT Ser	GGC Gly	ATC Ile 125	CTG Leu	CTG Leu	TTG Leu	GCC Ala	437
TGC Cys 130	ATC Ile	AGT Ser	GTG Val	GAC Asp	CGT Arg 135	TAC Tyr	CTG Leu	GCC Ala	ATT Ile	GTC Val 140	CAT His	GCC Ala	476
ACA Thr	CGC Arg	ACA Thr 145	CTG Leu	ACC Thr	CAG Gln	AAG Lys	CGT Arg 150	CAC His	TTG Leu	GTC Val	AAG Lys	TTT Phe 155	515
GTT Val	TGT Cys	CTT Leu	GGC Gly	TGC Cys 160	TGG Trp	GGA Gly	CTG Leu	TCT Ser	ATG Met 165	AAT Asn	CTG Leu	TCC Ser	554
CTG Leu	CCC Pro 170	TTC Phe	TTC Phe	CTT Leu	TTC Phe	CGC Arg 175	CAG Gln	GCT Ala	TAC Tyr	CAT His	CCA Pro 180	AAC Asn	593
AAT Asn	TCC s r	AGT Ser	CCA Pro 185	GTT Val	TGC Cys	ТАТ Туг	GAG Glu	GTC Val 190	Leu	GGA Gly	AAT Asn	GAC Asp	632
ACA Thr 195	GCA Ala	AAA Lys	TGG Trp	CGG Arg	ATG Met 200	Val	TTG Leu	Arg	Ile	CTG Leu 205	Pro	CAC His	671

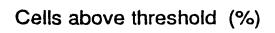
•

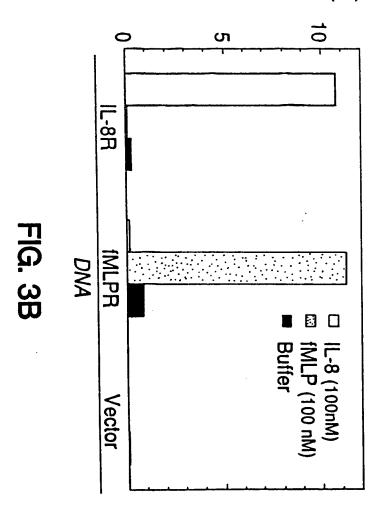
ACC TTT GGC TTC ATC GTG CCG CTG TTT GTC ATG CTG TTC 710 Thr Phe Gly Phe Ile Val Pro Leu Phe Val M t L u Phe 210 215 220
TGC TAT GGA TTC ACC CTG CGT ACA CTG TTT AAG GCC CAC 749 Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His 225 230
ATG GGG CAG AAG CAC CGA GCC ATG AGG GTC ATC TTT GCT 788 Met Gly Gln Lys His Arg Ala Met Arg Val Ile Phe Ala 235 240 245
GTC GTC CTC ATC TTC CTG CTT TGC TGG CTG CCC TAC AAC 827 Val Val Leu Ile Phe Leu Leu Cys Trp Leu Pro Tyr Asn 250 255
CTG GTC CTG CTG GCA GAC ACC CTC ATG AGG ACC CAG GTG 866 Leu Val Leu Ala Asp Thr Leu Met Arg Thr Gln Val 260 265 270
ATC CAG GAG ACC TGT GAG CGC CGC AAC AAC ATC GGC CGG 905 Ile Gln Glu Thr Cys Glu Arg Arg Asn Asn Ile Gly Arg 275 280 285
GCC CTG GAT GCC ACT GAG ATT CTG GGA TTT CTC CAT AGC 944 Ala Leu Asp Ala Thr Glu Ile Leu Gly Phe Leu His Ser 290 295
TGC CTC AAC CCC ATC ATC TAC GCC TTC ATC GGC CAA AAT 983 Cys Leu Asn Pro Ile Ile Tyr Ala Phe Ile Gly Gln Asn 300 305 310
TTT CGC CAT GGA TTC CTC AAG ATC CTG GCT ATG CAT GGC 1022 Phe Arg His Gly Phe Leu Lys Ile Leu Ala Met His Gly 315 320
CTG GTC AGC AAG GAG TTC TTG GCA CGT CAT CGT GTT ACC 1061 Leu Val Ser Lys Glu Phe Leu Ala Arg His Arg Val Thr 325 330 335
TCC TAC ACT TCT TCG TCT GTC AAT GTC TCT TCC AAC CTC 1100 Ser Tyr Thr Ser Ser Val Asn Val Ser Ser Asn Leu 340 345 350
TGAAAACCAT CGATGAAGGA ATATCTCTTC TCAGAAGGAA AGAATAACCA 1150
ACACCCTGAG GTTGTGTGT GAAGGTGATC TGGCTCTGGA CAGGCACTAT 1200
CTGGGTTTTG GGGGGACGCT ATAGGATGTG GGGAAGTTAG GAACTGGTGT 1250
CTTCAGGGGC CACACCAACC TTCTGAGGAG CTGTTGAGGT ACCTCCAAGG 1300
ACCGGCCTTT GCACCTCCAT GGAAACGAAG CACCATCATT CCCGTTGAAC 1350
GTCACATCTT TAACCCACTA ACTGGCTAAT TAGCATGGCC ACATCTGAGC 1400
CCCGAATCTG ACATTAGATG AGAGAACAGG GCTGAAGCTG TGTCCTCATG 1450

AGGGCTGGAT GCTCTCGTTG ACCCTCACAG GAGCATCTCC TCAACTCTGA 1500
GTGTTAAGCG TTGAGCCACC AAGCTGGTGG CTCTGTGTGC TCTGATCCGA 1550
GCTCAGGGGG GTGGTTTTCC CATCTCAGGT GTGTTGCAGT GTCTGCTGGA 1600
GACATTGAGG CAGGCACTGC CAAAACATCA ACCTGCCAGC TGGCCTTGTG 1650
AGGAGCTGGA AACACATGTT CCCCTTGGGG GTGGTGGATG AACAAAGAGA 1700
AAGAGGGTTT GGAAGCCAGA TCTATGCCAC AAGAACCCCC TTTACCCCCA 1750
TGACCAACAT CGCAGACACA TGTGCTGGCC ACCTGCTGAG CCCCAAGTGG 1800
AACGAGACAA GCAGCCCTTA GCCCTTCCCC TCTGCAGCTT CCAGGCTGGC 1850
GTGCAGCATC AGCATCCCTA GAAAGCCATG TGCAGCCACC AGTCCATTGG 1900
GCAGGCAGAT GTTCCTAATA AAGCTTCTGT TCC 1933

## FIG. 2C







TGC	rcca(	GTA (	GCCA	CCGC	AT C	rgga	GAACO	C AGO	CGGT	PACC	ATG Met 1	GAG Glu	96
GGG Gly	ATC Ile	AGT Ser 5	ATA Ile	TAC Tyr	ACT Thr	TCA Ser	GAT Asp 10	AAC Asn	TAC Tyr	ACC Thr	GAG Glu	GAA Glu 15	135
ATG Met	GGC Gly	TCA Ser	GGG Gly	GAC Asp 20	TAT Tyr	GAC Asp	TCC Ser	ATG Met	AAG Lys 25	GAA Glu	CCC Pro	TGT Cys	174
TTC Phe	CGT Arg 30	GAA Glu	GAA Glu	AAT Asn	GCT Ala	AAT Asn 35	TTC Phe	AAT Asn	AAA Lys	ATC Ile	TTC Phe 40	CTG Leu	213
CCC Pro	ACC Thr	ATC Ile	TAC Tyr 45	TCC Ser	ATC Ile	ATC Ile	TTC Phe	TTA Leu 50	ACT Thr	GGC Gly	ATT Ile	GTG Val	252
GGC Gly 55	AAT Asn	GGA Gly	TTG Leu	GTC Val	ATC Ile 60	CTG Leu	GTC Val	ATG Met	GGT Gly	TAC Tyr 65	CAG Gln	AAG Lys	291
AAA Lys	CTG Leu	AGA Arg 70	AGC Ser	ATG Met	ACG Thr	GAC Asp	AAG Lys 75	TAC Tyr	AGG Arg	CTG Leu	CAC His	CTG Leu 80	330
TCA Ser	GTG Val	GCC Ala	Asp	CTC Leu 85	CTC Leu	TTT Phe	GTC Val	ATC Ile	ACG Thr 90	CTT Leu	CCC Pro	TTC Phe	369
TGG Trp	GCA Ala 95	GTT Val	GAT Asp	GCC Ala	GTG Val	GCA Ala 100	AAC Asn	TGG Trp	TAC Tyr	TTT Phe	GGG Gly 105	AAC Asn	408
TTC Phe	CTA Leu	TGC Cys	AAG Lys 110	GCA Ala	GTC Val	CAT His	GTC Val	ATC Ile 115	TAC Tyr	ACA Thr	GTC Val	AAC Asn	447
CTC Leu 120	TAC Tyr	AGC Ser	AGT Ser	GTC Val	CTC Leu 125	ATC Ile	CTG Leu	GCC Ala	TTC Phe	ATC Ile 130	AGT Ser	CTG Leu	486
GAC Asp	CGC Arg	TAC Tyr 135	CTG Leu	GCC Ala	ATC Ile	GTC Val	CAC His 140	GCC Ala	ACC Thr	AAC Asn	AGT Ser	CAG Gln 145	525
AGG Arg	CCA Pro	AGG Arg	AAG Lys	CTG Leu 150	TTG Leu	GCT Ala	GAA Glu	AAG Lys	GTG Val 155	GTC Val	TAT Tyr	GTT Val	564
GGC Gly	GTC Val 160	TGG Trp	ATC Ile	CCT Pro	GCC Ala	CTC Leu 165	CTG Leu	CTG Leu	ACT Thr	ATT Ile	CCC Pro 170	GAC Asp	603
TTC Phe	ATC Ile	TTT Phe	GCC Ala 175	AAC Asn	GTC Val	Ser	GAG Glu	Ala 180	Asp	GAC Asp	AGA Arg	TAT Tyr	642

FIG. 4A

ATC Ile 185	TGT Cys	GAC Asp	CGC Arg	TTC Ph	TAC Tyr 190	CCC Pro	AAT Asn	GAC Asp	TTG Leu	TGG Trp 195	GTG Val	GTT Val	681	
GTG Val	TTC Phe	CAG Gln 200	TTT Phe	CAG Gln	CAC His	ATC Ile	ATG Met 205	GTT Val	GGC Gly	CTT Leu	ATC Ile	CTG Leu 210	720	
CCT Pro	GGT Gly	ATT Ile	GTC Val	ATC Ile 215	CTG Leu	TCC Ser	TGC Cys	TAT Tyr	TGC Cys 220	ATT Ile	ATC Ile	ATC Ile	759	
TCC Ser	AAG Lys 225	CTG Leu	TCA Ser	CAC His	TCC Ser	AAG Lys 230	GGC Gly	CAC His	CAG Gln	AAG Lys	CGC Arg 235	AAG Lys	798	
GCC Ala	CTC Leu	AAG Lys	ACC Thr 240	ACA Thr	GTC Val	ATC Ile	CTC Leu	ATC Ile 245	CTG Leu	GCT Ala	TTC Phe	TTC Phe	837	
GCC Ala 250	TGT Cys	TGG Trp	CTG Leu	CCT Pro	TAC Tyr 255	TAC Tyr	ATT Ile	GGG Gly	ATC Ile	AGC Ser 260	TTE	GAC Asp	876	
TCC Ser	TTC Phe	ATC Ile 265	CTC Leu	CTG Leu	GAA Glu	ATC Ile	ATC Ile 270	AAG Lys	CAA Gln	GGG Gly	TGT Cys	GAG Glu 275	915	
TTT Phe	GAG Glu	AAC Asn	ACT Thr	GTG Val 280	CAC His	AAG Lys	TGG Trp	ATT Ile	TCC Ser 285	ATC Ile	ACC Thr	GAG Glu	954	
GCC Ala	CTA Leu 290	Ala	TTC Phe		CAC His	TGT Cys 295	Cys	CTG Leu	AAC Asn	CCC Pro	ATC Ile 300	Leu	993	
TAT Tyr	GCT Ala	TTC Phe	CTT Leu 305	GGA Gly	GCC Ala	AAA Lys	TTT Phe	AAA Lys 310	Thr	TCT	GCC Ala	CAG Gln	103	2
CAC His 315	Ala	CTC Leu	ACC Thr	TCT Ser	GTG Val 320	AGC Ser	AGA Arg	GGG Gly	Ser	AGC Ser 325	Leu	AAG Lys	107	1
ATC Ile	CTC Leu	TCC Ser 330	Lys	GGA Gly	AAG Lys	CGA Arg	GGT Gly 335	Gly	CAT His	TCA Ser	TCT Ser	GTT Val	111	.0
TCC Ser	ACT Thr	GAG Glu	TCT	GAG Glu 345	Ser	TCA Ser	AGT Ser	TTT Phe	CAC His	Ser	Ser 352		AC 11	.50
ACA	GATG	TAA	AAGA	CTTT	тт т	TAT	ACGA	T ÄÄ	ATAA	CTTI	TTT	TTA	GTT	1200
ACA	.CATT	TTT	CAGA	ATAT.	AA A	GACI	GACC	TA AS	ATTG	TACA	GTT	TTTT	ATTG	1250
CTT	GTTG	GAT	TTTI	GTCT	TG I	GTTI	CTTI	'A GI	TTTT	GTGA	AGT	ATT	ATTG	1300
CTTGTTGGAT TTTTGTCTTG TGTTTCTTTA GTTTTTGTGA AGTTTAATTG 130  ACTTATTTAT ATAAATTTTT TTTGTTTCAT ATTGATGTGT GTCTAGGCAG 135  FIG. 4B													GCAG	1350

FIG. 4C

GAAT	TCCA	GT G	TGCT	عاعات	G CC	GCCC.	VGIG	160	1660		- CON			•
GGAA	AGGA	CA G	AGGT	TATG	A GT	GCCT	GCAA	GAG	TGGC	AGC	CTGG	AGTA(	GA 1	100
GAAA	ACAC	TA A	AGGI	'GGAG	T CA	AAAG	ACCT	GAG	TTCA	AGT	CCCA	GCTC'	TG :	150
CCAC	TGGI	TA G	CTGI	GGGA	т ст	CGGA	AAAG	ACC	CAGT	GAA	AAAA	AAAA	AA :	200
AAAG	TGAT	GA G	TTGI	GAGG	C AG	GTCG	CGGC	CCT	ACTG	CCT	CAGG	AGAC	GA :	250
TGCGCAGCTC ATTTGCTTAA ATTTGCAGCT GACGGCTGCC ACCTCTCTAG 300														
AGGCACCTGG CGGGGAGCCT CTCAACATAA GACAGTGACC AGTCTGGTGA 350														
CTC#	ACAGO	ccs (	GCAC?	AGCC	ATG Met 1	AAC Asn	TAC Tyr	CCG Pro	CTA Leu 5	ACG Thr	CTG Leu	GAA Glu	392	
ATG Met	GAC Asp 10	CTC Leu	GAG Glu	AAC Asn	CTG Leu	GAG Glu 15	GAC Asp	CTG Leu	TTC Phe	TGG Trp	GAA Glu 20	CTG Leu	431	
GAC Asp	AGA Arg	TTG Leu	GAC Asp 25	AAC Asn	TAT Tyr	AAC Asn	GAC Asp	ACC Thr 30	TCC Ser	CTG Leu	GTG Val	GAA Glu	470	ı
AAT Asn 35	CAT His	CTC Leu	TGC Cys	CCT Pro	GCC Ala 40	ACA Thr	GAG Glu	GGĢ Gly	CCC Pro	CTC Leu 45	ATG Met	GCC Ala	509	ı
TCC Ser	TTC Phe	Lys	GCC Ala	GTG Val	TTC Phe	GTG Val	CCC Pro	GTG Val	GCC Ala	TAC Tyr	AGC Ser	CTC Leu 60	548	3
ATC Ile	TTC Phe	50 CTC Leu	CTG Leu	GGC Gly 65	GTG Val	ATC Ile	GGC	AAC Asn	GTC Val 70	CTG Leu	GTG Val	CTG Leu	587	
Val	Ile 75	Leu	GAG Glu	Arg	His	80	GIN	THE	Arg	Ser	85	1111		
Glu	Thr	Phe	CTG Leu 90	Phe	His	Leu	Ala	95	Ala	кэр	Dea	Дец		
Leu 100	Val	Phe	ATC Ile	Leu	Pro 105	Pne	Ala	Val	Ara	110	Gly	Der		
Val	Gly	Trp 115		Leu	GIY	Thr	120	Leu	Суб	гЛэ	1111	125		
ATT Ile	GCC Ala	CTG Leu	CAC His	AAA Lys 130	Val	Asn	TTC Phe	туг	TGC Cys 135	AGC Ser	AGC Ser	CTG Leu	782	2
							~ ~							

	Leu 140	Ala	Cys	Ile A	Ala	Val . 145	Asp	Arg	Tyr	Leu	150	116		
	His	Ala	Val 155	His .	Ala	Tyr	Arg	160	Arg	Arg	Leu .	Leu		
Ser 165	Ile	His	Ile	Thr	Cys 170	Gly	Thr	IIe	Trp	175	GTG Val	GIY		
Phe	Leu	Leu 180	Ala	Leu	Pro	GIU	11e 185	Leu	Pne	ATG	AAA Lys	190		
Ser	Gln	Gly	His	His 195	Asn	Asn	ser	Leu	200	Arg	TGC Cys	1111		
Phe	Ser 205	Gln	Glu	Asn	Gln	210	Glu	Thr	nis	ATG	215	FIIC	1016	
Thr	Ser	Arg	Phe 220	Leu	Tyr	His	vaı	225	GIY	Pne	Den	Dea	1055	
Pro 230	Met	Leu	Val	Met	G1y 235	Trp	Cys	TYE	Val	240	Vul	<b>V U L</b>	1094	
His	Arg	Leu 245	Arg	Gln	Ala	GIN	250	Arg	PIO	GIII	nry	255	1133	
Lys	Ala	Val	Arg	Val 260	Ala	11e	Leu	Val	265	Ser	110		1172	
Phe	Leu 270	Cys	Trp	Ser	Pro	1yr 275	nıs	116	val	116	280	200	1211	
Asp	Thr	Leu	Ala 285	Arg	Leu	гÀг	Ala	290	vəh	, KSII		o <sub>j</sub> -	1250	-
Lys 295	Leu	Asn	Gly	Ser	300	Pro	Val	MIG	, 116	305	1100	0,10		
Glu	Phe	Leu 310	Gly	Leu	Ala	HIS	315	. Cys	. Dec	, ASI		320		
Leu	Tyr	Thr	Ph	Ala 325	GIY	vaı	. Lys	s Pile	330	)	. nop	, ,		
TCG Ser	CGG Arg 335	Lev	CTG Lev	ACG Thr	AAG Lys	CTG Lev 340	r GTŽ	TGT CYS	> 1111	L GI	C CCT y Pro 345		2 1406	
							ı		. –					

TCC CTG TGC CAG CTC TTC CCT AGC TGG CGC AGG AGC AGT 1445 Ser Leu Cys Gln Leu Phe Pro Ser Trp Arg Arg Ser Ser 350 355

CTC TCT GAG TCA GAG AAT GCC ACC TCT CTC ACC ACG TTC TA 1486 Leu Ser Glu Ser Glu Asn Ala Thr Ser Leu Thr Thr Phe 360 365 370 372

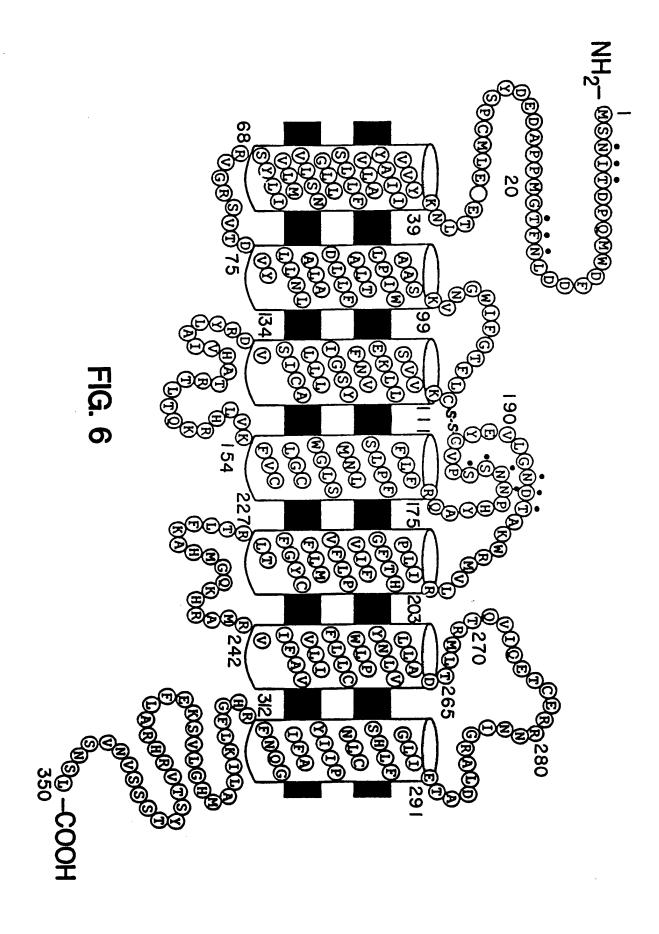
GGTC CCAGTGTCCC CTTTTATTGC TGCTTTTCCT TGGGGCAGGC 1530

AGTGATGCTG GATGCTCCTT CCAACAGGAG CTGGGATCCT AAGGGCTCAC 1580

CGTGGCTAAG AGTGTCCTAG GAGTATCCTC ATTTGGGGTA GCTAGAGGAA 1630

CCAACCCCA TTTCTAGAAC ATCCCGCGGC CGCCAGCACA CTGGAATTC 1679

FIG. 5C



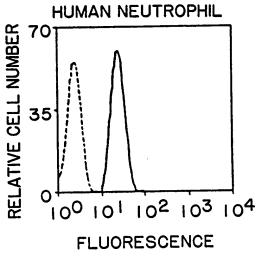


FIG. 7A

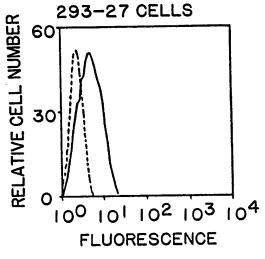


FIG. 7B

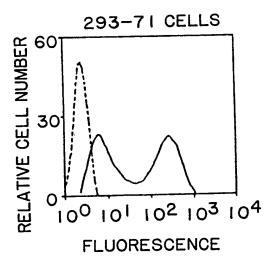


FIG. 7C

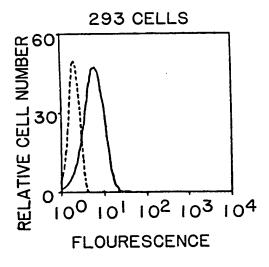
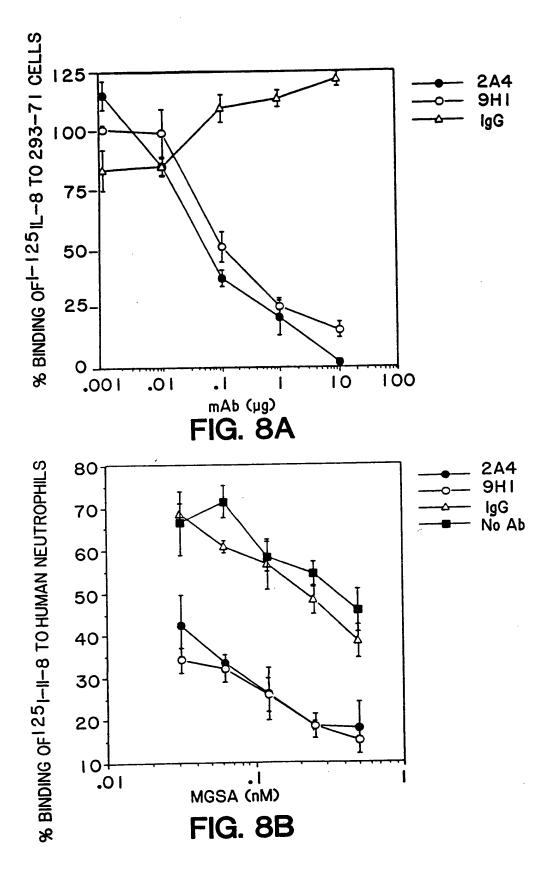


FIG. 7D



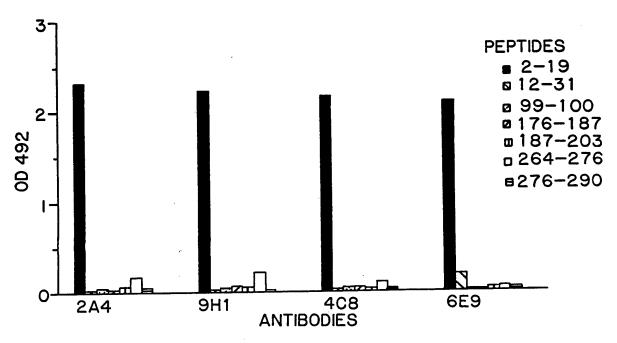


FIG. 9A

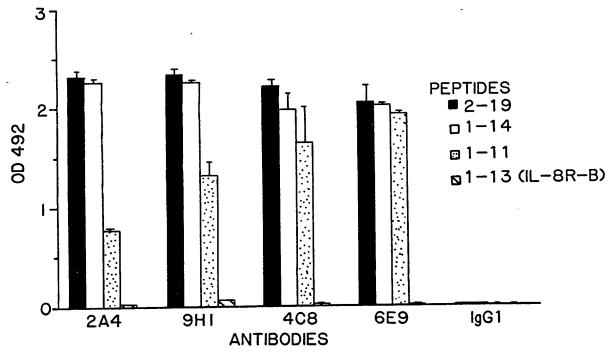


FIG. 9B

